

Computation of summary statistics, S, Pi, H12, and LD

NG Nandita R. Garud DP Dmitri A. Petrov

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 An abbreviated version of this protocol was published in PLoS Genetics in Feb 2021
Detection of hard and soft selective sweeps from *Drosophila melanogaster* population genomic data
DOI: 10.1371/journal.pgen.1009373

Detailed protocol

Hello,

Would you please consider consulting our code on github for computing H12?

<https://github.com/ngarud/SelectionHapStats>

Best wishes,
Nandita

How to cite: (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Garud, N. and Petrov, D. (2023). Computation of summary statistics, S, Pi, H12, and LD. Bio-protocol Preprint. bio-protocol.org/prep2123.
2. Garud, N. R., Messer, P. W. and Petrov, D. A. (2021). Detection of hard and soft selective sweeps from *Drosophila melanogaster* population genomic data. PLoS Genetics 17(2). DOI: [10.1371/journal.pgen.1009373](https://doi.org/10.1371/journal.pgen.1009373)

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